

(PRIOR ART)

Figure 1

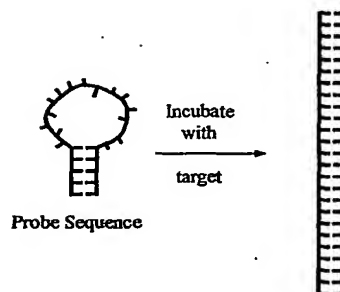


Figure 2

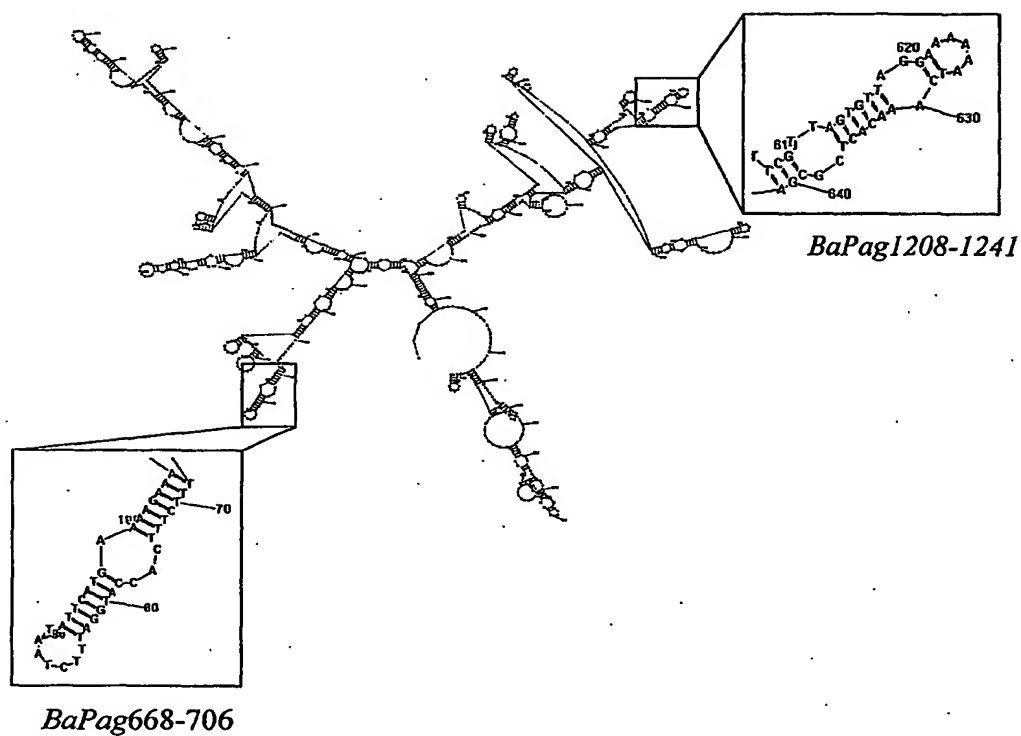


Figure 3

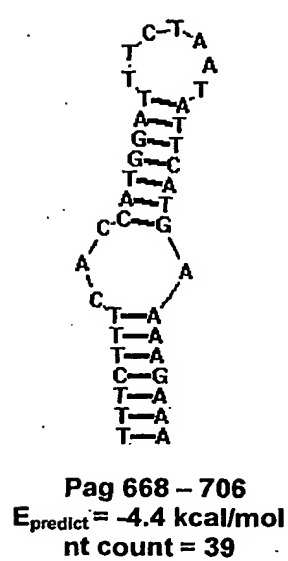


Figure 4A

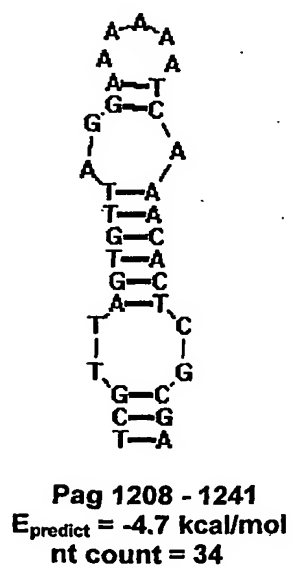


Figure 4B

Sequences producing significant alignments:		Score (bits)	E Value
<u>gi 20520075 gb AF011190.1 </u>	<u>Bacillus anthracis str. A2012 pl...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 16031494 emb J7413937.1 BAN413937</u>	<u>Bacillus anthracis par...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 16031492 emb J7413936.1 BAN413936</u>	<u>Bacillus anthracis par...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 9280592 gb AF268967.1 AF268967</u>	<u>Bacillus anthracis plasmid...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 4894216 gb AF065404.1 </u>	<u>Bacillus anthracis virulence plas...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 10880952 gb AF306783.1 </u>	<u>Bacillus anthracis isolate BA102...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 10880950 gb AF306782.1 </u>	<u>Bacillus anthracis plasmid pX01 ...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 10880948 gb AF306781.1 </u>	<u>Bacillus anthracis isolate 33 pr...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 10880946 gb AF306780.1 </u>	<u>Bacillus anthracis isolate BA103...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 10880944 gb AF306779.1 </u>	<u>Bacillus anthracis isolate 28 pr...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 10880942 gb AF306778.1 </u>	<u>Bacillus anthracis plasmid pX01 ...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 143280 gb M22589.1 BACFAG</u>	<u>Bacillus anthracis cryptic pro...</u>	<u>78</u>	<u>7e-13</u>
<u>gi 18308294 gb AC104301.2 </u>	<u>Homo sapiens chromosome 3 clone ...</u>	<u>42</u>	<u>0.038</u>
<u>gi 13033969 gb AC069286.7 </u>	<u>Homo sapiens BAC clone RP11-261N...</u>	<u>40</u>	<u>0.15</u>
<u>gi 34849950 gb AC107065.5 </u>	<u>Bos taurus clone rp42-513q13, co...</u>	<u>40</u>	<u>0.15</u>
<u>gi 30962756 gb AC137820.11 </u>	<u>Medicago truncatula clone mth2-...</u>	<u>38</u>	<u>0.60</u>
<u>gi 30522931 gb AC123948.4 </u>	<u>Mus musculus chromosome 10 clone...</u>	<u>38</u>	<u>0.60</u>
<u>gi 22552809 emb AL671857.16 </u>	<u>Mouse DNA sequence from clone ...</u>	<u>38</u>	<u>0.60</u>
<u>gi 11414843 emb L355352.16 </u>	<u>Human DNA sequence from clone ...</u>	<u>38</u>	<u>0.60</u>
<u>gi 7768715 dbj AF001713.1 </u>	<u>Homo sapiens genomic DNA, chromo...</u>	<u>38</u>	<u>0.60</u>
<u>gi 4827077 dbj AF000178.1 </u>	<u>Homo sapiens genomic DNA, chromo...</u>	<u>38</u>	<u>0.60</u>
<u>gi 4835635 dbj AF000266.1 </u>	<u>Homo sapiens genomic DNA, chromo...</u>	<u>38</u>	<u>0.60</u>
<u>gi 3132344 dbj AF000034.1 </u>	<u>Homo sapiens genomic DNA, chromo...</u>	<u>38</u>	<u>0.60</u>
<u>gi 4730836 dbj AF000102.1 </u>	<u>Homo sapiens genomic DNA of 21q2...</u>	<u>38</u>	<u>0.60</u>
<u>gi 3947430 gb AC003090.1 </u>	<u>Homo sapiens BAC clone CIA-241I2 ...</u>	<u>36</u>	<u>2.4</u>

Figure 5

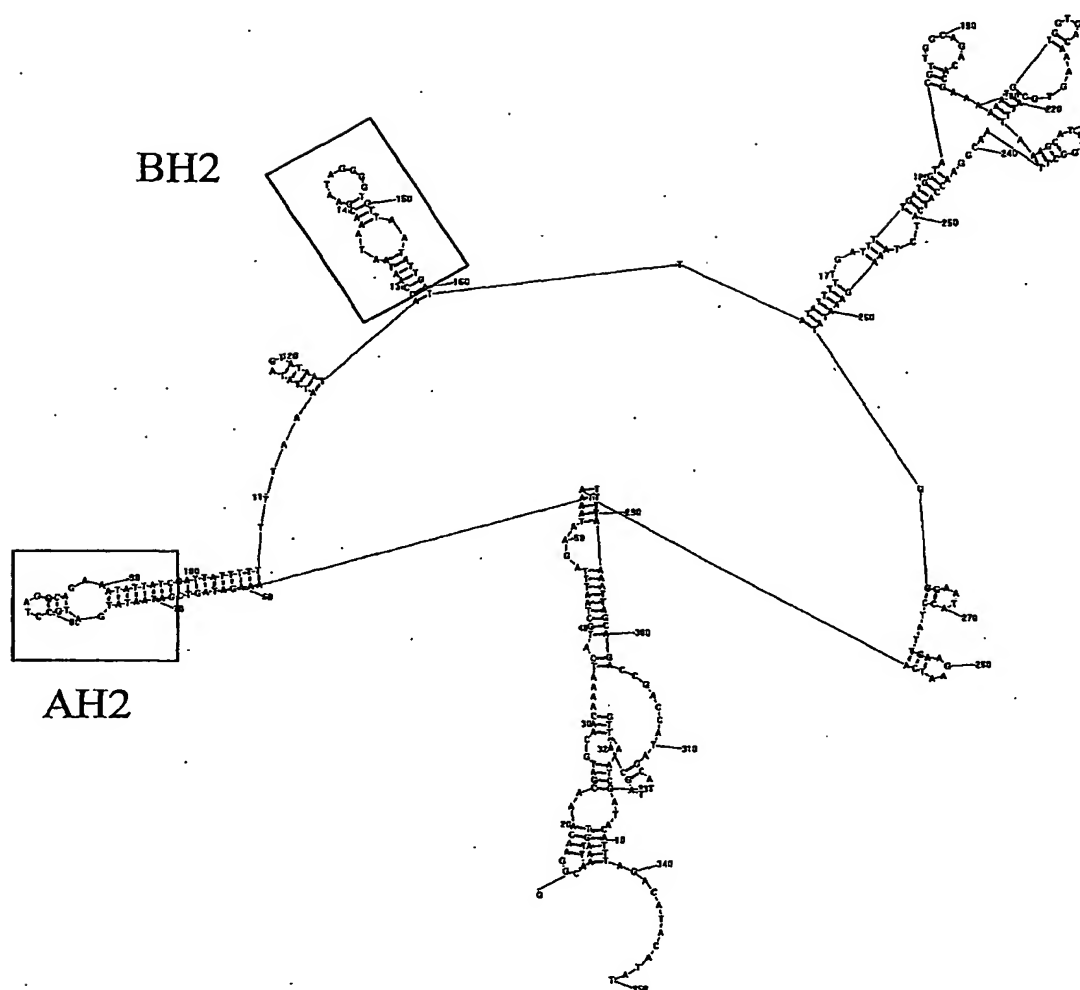


Figure 6

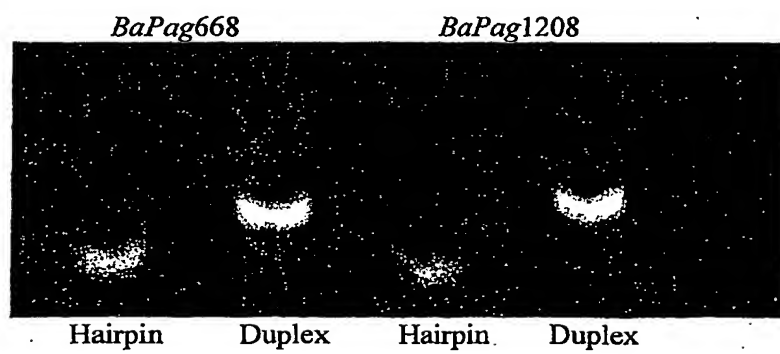


Figure 9

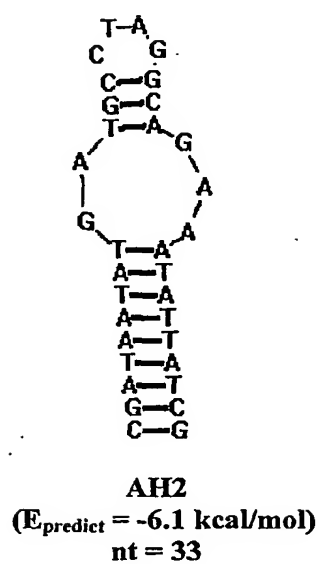


Figure 7A

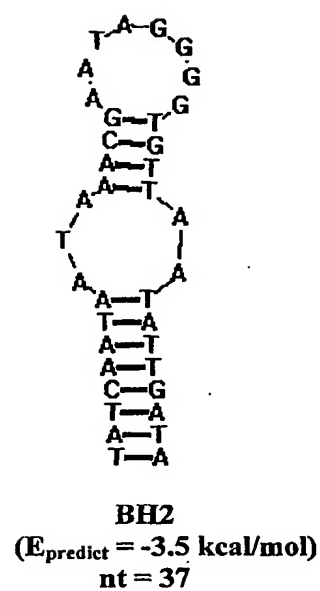
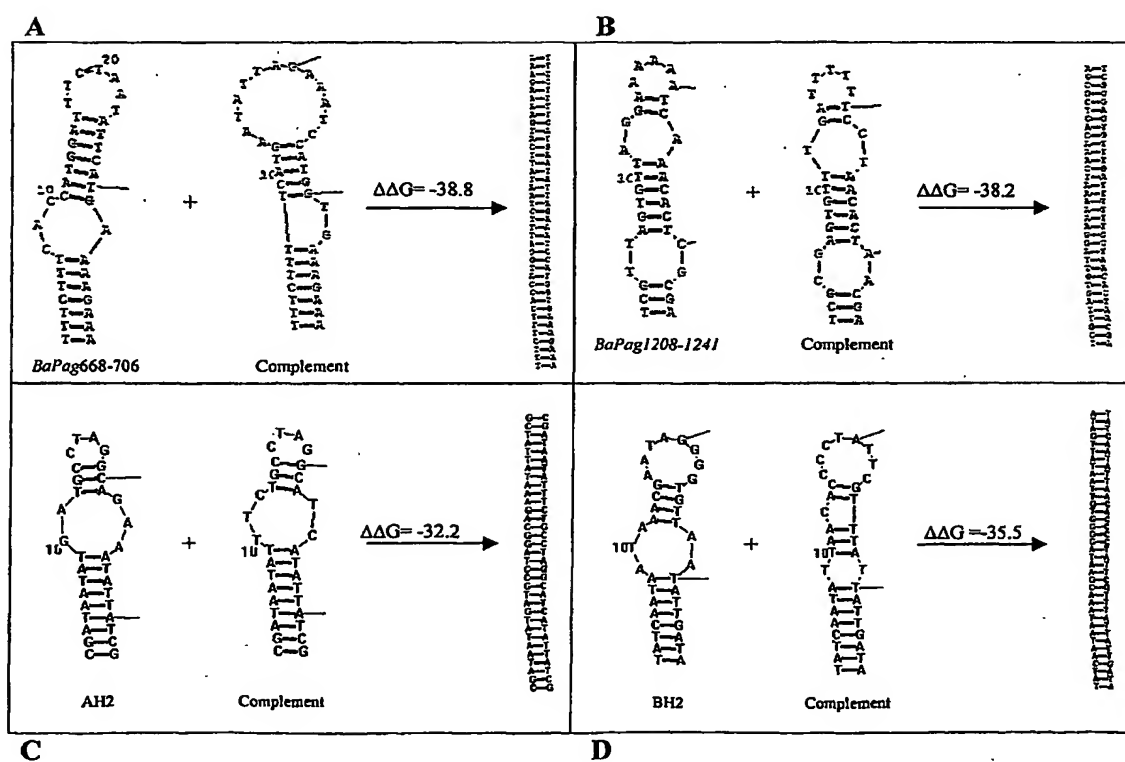
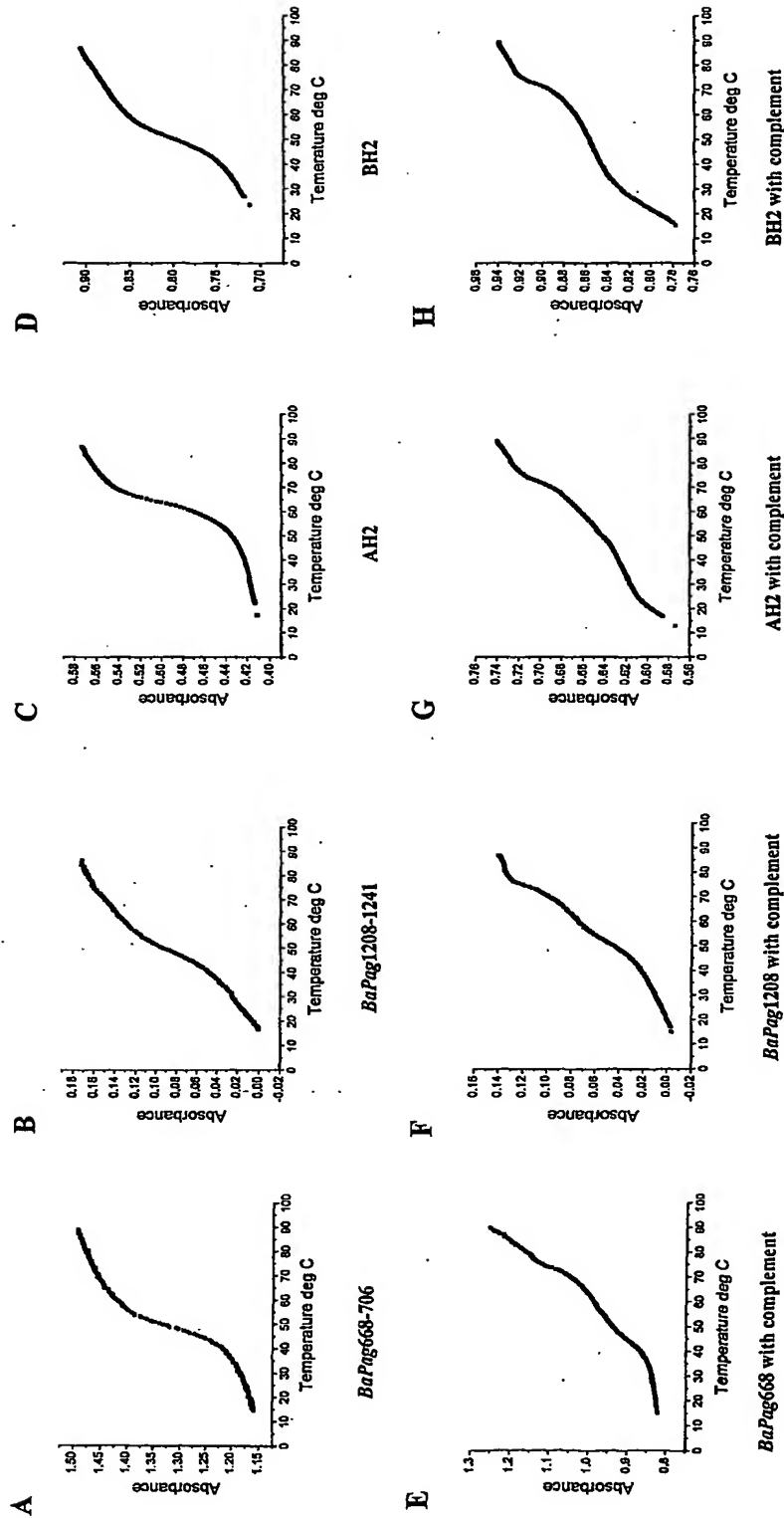


Figure 7B



Figures 8A-D



Figures 10A-H

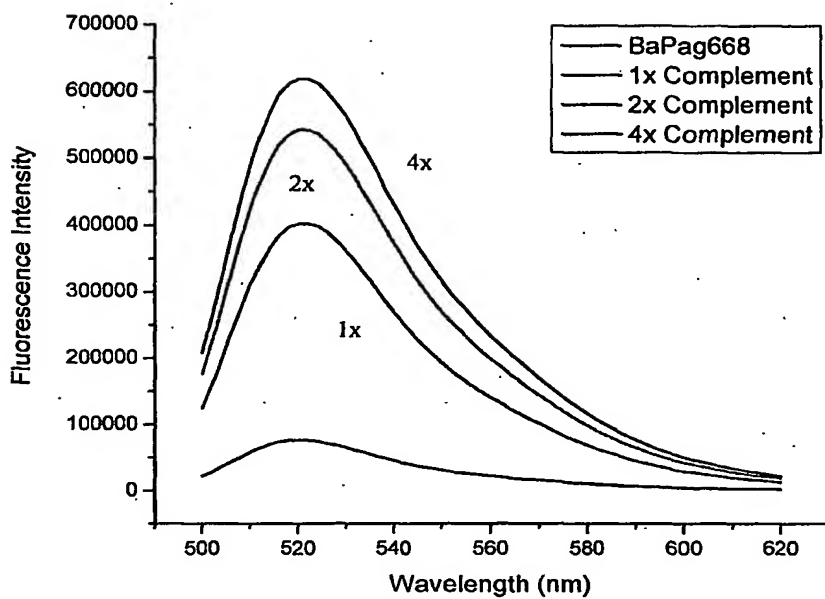
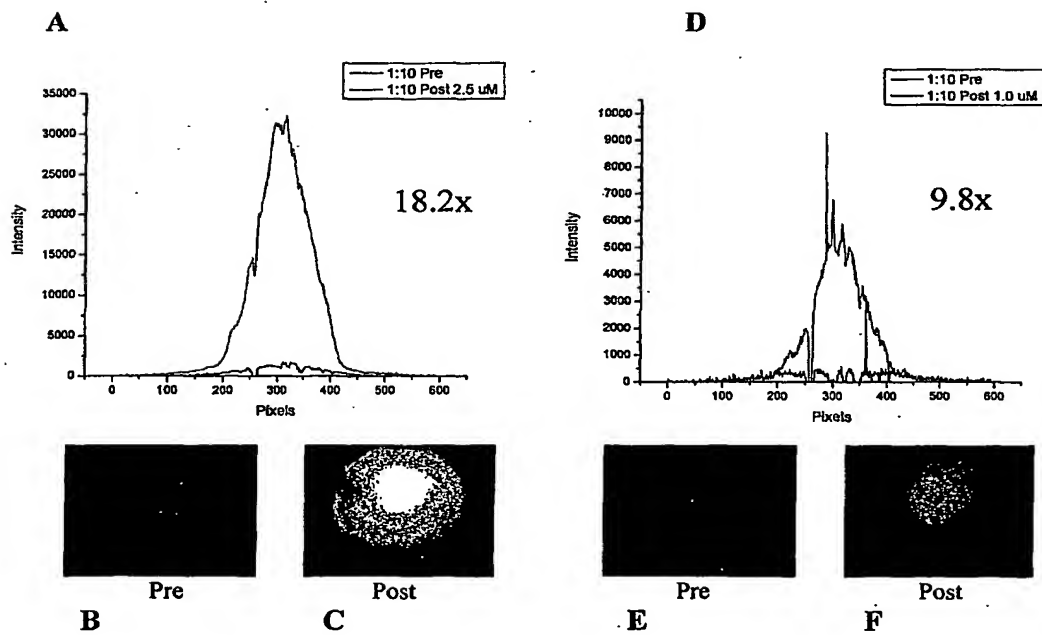
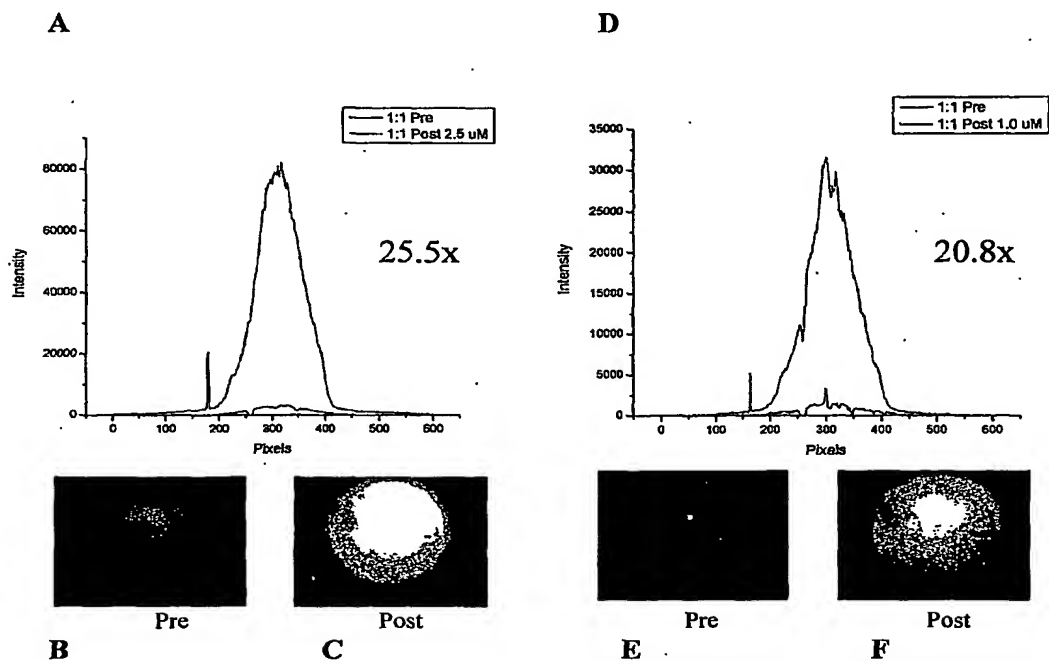


Figure 11



Figures 12A-F



Figures 13A-F

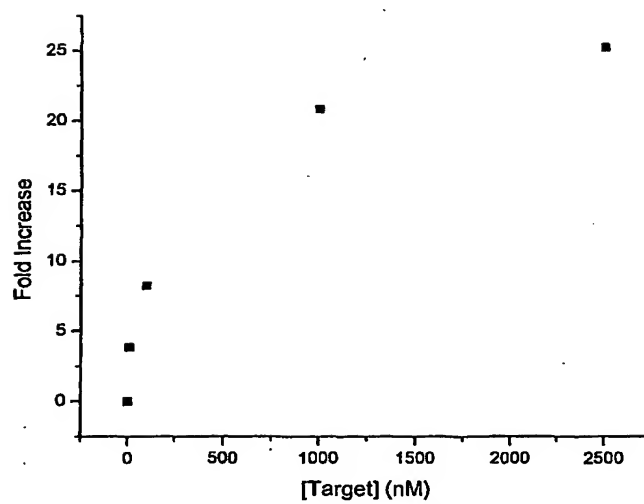
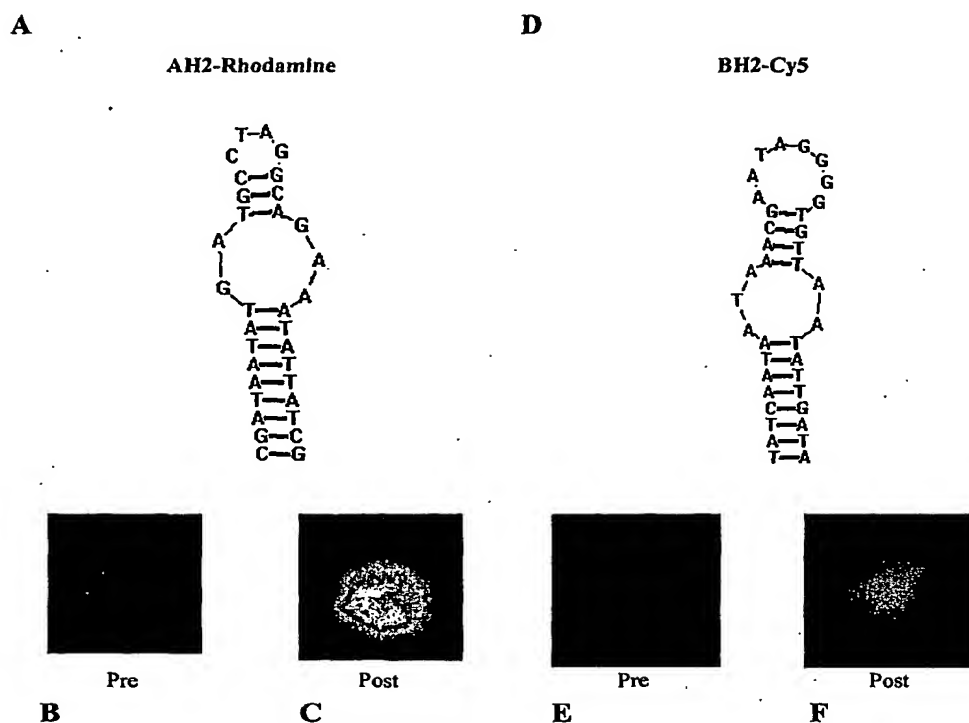



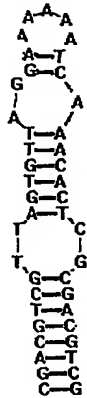

Figure 14



Figures 15A-F

A	B	C
<i>BaPag668</i>	<i>BaPag668 + CGACG</i>	<i>BaPag673 + CGACG</i>
$\Delta G_{hp} = -4.4$	$\Delta G_{hp} = -12.9$	$\Delta G_{hp} = -7.3$
$\Delta G_{dup} = -43.2$	$\Delta G_{dup} = -43.2$	$\Delta G_{dup} = -32.5$
$\Delta \Delta G = -38.8$	$\Delta \Delta G = -30.3$	$\Delta \Delta G = -25.2$
Complement: TTTCT TTTCA TGAAT ATTAG AAATC CATGG TGAAA GAAA		

Figures 16A-C

A	B	C
		
<i>BaPag1208</i>	<i>BaPag1208 + CGACG</i>	<i>BaPag1213 + CGACG</i>
$\Delta G_{bp} = -4.7$	$\Delta G_{bp} = -13.2$	$\Delta G_{bp} = -11.3$
$\Delta G_{dup} = -42.6$	$\Delta G_{dup} = -42.8$	$\Delta G_{dup} = -33.7$
$\Delta \Delta G = -38.2$	$\Delta \Delta G = -29.6$	$\Delta \Delta G = -22.4$
Complement: TCGCG AGTGT TTGAT TTTT CCTAA CACTA ACGA		

Figures 17A-C